FIGURE 1

TGMV Rep, amino acids 110-179:

TLVWGEFQVD GRSARGGCQT S<u>NDAAAEALN</u> ASS<u>KEEALQI IRE</u>KIPEKYL FQFHNLNSNL DRIFDKTPEP (SEQ ID NO:2)

Ala 1 mutant:

TLVWGEFQVD G<u>AA</u>A<u>A</u>GGCQT S<u>NDAAAEALN</u> ASS<u>KEEALQI IRE</u>KIPEKYL FQFHNLNSNL DRIFDKTPEP (SEQ ID NO:3)

Ala5 mutant:

TLVWGEFQVD GRSARGGCQT S<u>NDAAAEALN</u> ASS<u>AAALQI IRE</u>KIPEKYL FQFHNLNSNL DRIFDKTPEP (SEQ ID NO:15)

Ala4+5 mutant:

TLVWGEFQVD GRSARGGCQT S<u>NDAAAAALA</u> ASS<u>AAAALOI IRE</u>KIPEKYL FQFHNLNSNL DRIFDKTPEP (SEQ ID NO:4)

Ala6 mutant:

TLVWGEFQVD GRSARGGCQT S<u>NDAAAEALN</u> ASS<u>KEEALQI IAAA</u>IPEKYL FQFHNLNSNL DRIFDKTPEP (SEQ ID NO:5)

Ala7 mutant:

TLVWGEFQVD GRSARGGCQT S<u>NDAAAEALN</u> ASS<u>KEEALQI IRE</u>KIP<u>AAA</u>L FQFHNLNSNL DRIFDKTPEP (SEQ ID NO:6)

Ala8 mutant:

TLVWGEFQVD GRSARGGCQT S<u>NDAAAEALN</u> ASS<u>KEEALQI IRE</u>KIPEKYL F<u>AFAA</u>LNSNL DRIFDKTPEP (SEQ ID NO:7)

Ala9 mutant:

TLVWGEFQVD GRSARGGCQT S<u>NDAAAEALN</u> ASS<u>KEEALQI IRE</u>KIPEKYL FQFHNLNS<u>A</u>L <u>AA</u>IFDKTPEP (SEQ ID NO:8)

Ala13 mutant:

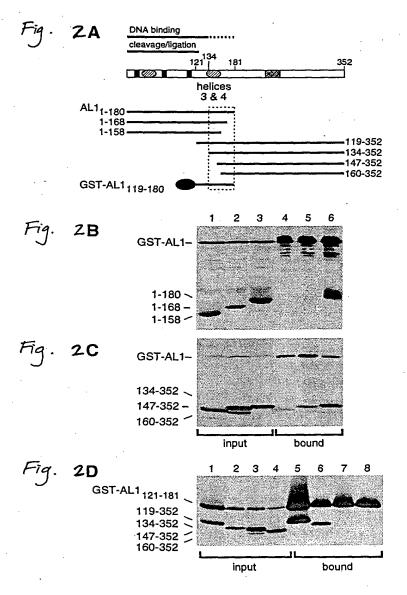
TLVWGE<u>AA</u>VD GRSARGGCQT S<u>NDAAAEALN</u> ASS<u>KEEALQI IRE</u>KIPEKYL FQFHNLNSNL DRIFDKTPEP (SEQ ID NO:9)

Ala14 mutant:

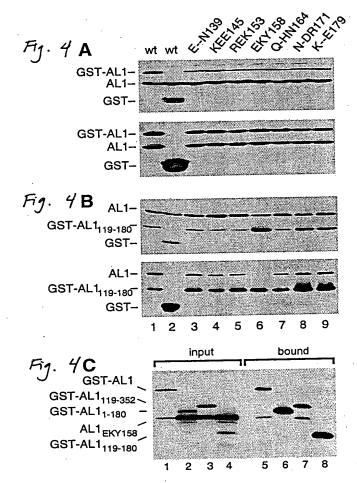
TLVWGEFQV<u>A</u> GRSARGGCQT S<u>NDAAAEALN</u> ASS<u>KEEALQI IRE</u>KIPEKYL FQFHNLNSNL DRIFDKTPEP (SEQ ID NO:10)

Leu mutant:

TLVWGEFQVD GRSARGGCQT S<u>NDLLLEALN</u> ASS<u>KEEALQI IRE</u>KIPEKYL FQFHNLNSNL DRIFDKTPEP (SEQ ID NO:11)

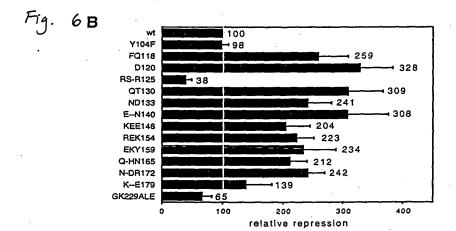


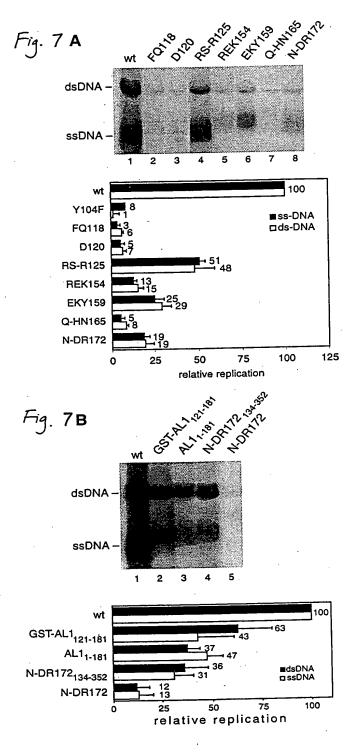
FQ118 D120 RS-R125 QT130 ND133 E---N140 KEE146 REK154 EKY159 Q--HN165 N--DR172 K---E179 WIID 1900 GEFOVDGRSARGGCOTSNDAAAEALNASSKEEALQIIREKIPEKYLFOFHNLNSNLDRIFDKTPEP helix 3 helix 4 core oligomerization domain Æ 180 — AL1/AL1 TPEP +++ +++ +++ +++ +++ +++

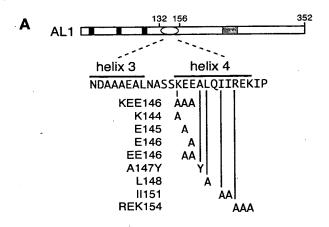


REK154 EKY-159 0 Q-HN165 wild type FQ118 D120 RS-R125 R122 S123 R125 QT130 ND133 AAA136 E-N140 KEE146 6 60 80 AL1/AL1 (rel. int.) 8 T ē 120 140 REKY-159 Q-HN165 N-DR172 K--E179 wild type FQ118 D120 RS-R125 0.5 R122 S123 R125 QT130 ND133 AAA136 E-N140 KEE146 6 60 80 100 AL 1/mRb (rel. int.) T 1 107 120 140 135

160







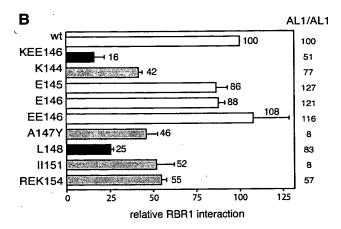


Fig. 9

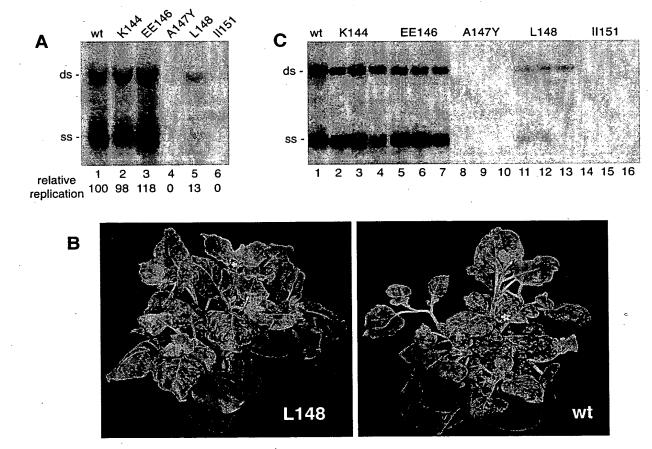
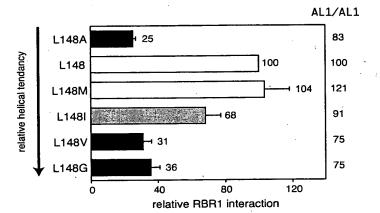
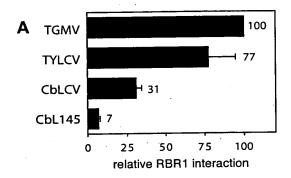


Fig.10





Helix 4
TGMV KEEALQIIREKIP
TYLCV-DR KSEALKILRELAP
CbLCV VEEALAIIRAGDP
consensus (±)₁₋₃ ALXIIREXXP
D